

Table III

Gene Name	Coriell IDNA Panel(s)	Amplicon No.	Total SNPs	Missense	Silent	UTR	Intronic
Aminopeptidase P (XPNPEP2)	24 + 47 (55AA) +12pt	24	30	0	2	7	21
Bradykinin B1 receptor (BDKRB1)	24+ 95 (8AA, 103 CAU) +12pt	7	14	2	5	3	4
Bradykinin B2 receptor (BDKRB2)	24 (8AA) +12pt	12	36	3	2	14	17
NK1 tachykinin receptor (TACR1)	24 (8AA) +12pt	7	9	0	3	3	3
C1 esterase inhibitor (C1NH)	24 (8AA) +12pt	10	6	2	2	0	2
Kallikrein 1 (KLK1)	7 (7AA) +12pt	5	6	1	1	2	2
Protease Inhibitor 4 (PI4)	7 (7AA) +12pt	8	12	1	3	1	7
Angiotensin Converting Enzyme 2 (ACE2)	7 (7AA) +12pt	20	9	0	0	0	9
Totals:			122	9	18	30	65

Table IV (1 of 2)

Table IV (2 of 2)

Table V (Top 2)

Table V (2 of 2)

GENE DESCRIPTION	GENC ID	SNP ID	CONTIG, NUM	CONTIG, POS	REF_AA	ALT_AA	EXON	MUTATION_TYPE	REF_CODON	ALT_CODON	PROTEIN_ID	PROTEIN_POS	PROTEIN SEQ ID	FLANK SEQ ID	FLANK SEQ REF	FLANK SEQ ID	REFSEQ, FLANK REF	
Aminopeptidase P (membrane-bound)	XENPEP2	AE10081	1	127	P	P	Exon20	Silent	0	CCC	AABRE3941	607	4	37	100	163		
Bradykinin Receptor B1	BDKRB1	AE10381	6	307	R	Q	Exon2	Missense	0	CAG	NP_000701.1	317	8	60	123	186		
Bradykinin Receptor B1	BDKRB1	AE10382	4	273	P	P	Exon2	Silent	0	CCG	NP_000701.1	41	10	61	124	187		
Tachykinin Receptor 1	TACR1	AE10851	1	614	F	F	Exon1	Silent	1	TTT	NP_0010481	111	16	81	144	207		
Tachykinin Receptor 1	TACR1	AE10852	2	769	I	I	Exon2	Silent	1	ATC	ATA	NP_0010481	154	18	82	145	208	
Tachykinin Receptor 1	TACR1	AE10867	6	511	S	S	Exon5	Silent	1	TCA	TCA	NP_0010481	378	20	87	150	213	
C1 Esterase Inhibitor	C1NH	AE10583	5	366	S	S	Exon7	Silent	0	AGC	AAT	NP_0006531	406	24	90	153	216	
C1 Esterase Inhibitor	C1NH	AE10584	7	586	V	A	Exon3	Missense	0	GTT	GCT	NP_0006531	56	26	91	154	217	
C1 Esterase Inhibitor	C1NH	AE10585	7	897	A	G	Exon3	Missense	0	GCA	GCA	NP_0006531	159	26	92	155	218	
C1 Esterase Inhibitor	C1NH	AE10586	8	276	V	M	Exon8	Missense	0	GTC	ATG	NP_0006531	480	30	93	156	219	
Kallikrein 1 (renin/angiotensin/kinin)	KLK1	AE10781	1	153	K	E	Exon4	Missense	0	AAA	AAA	NP_002248.1	186	34	94	157	220	
Kallikrein 1 (renin/angiotensin/kinin)	KLK1	AE10783	2	605	E	Q	Exon3	Missense	0	GAG	CAG	NP_002248.1	145	36	96	159	222	
Bradykinin Receptor B1	BDKRB1	AE10388	1	97	N	N	Exon3	Silent	0	AAC	AAT	NP_000701.1	114	556	579	611	643	
Bradykinin Receptor B1	BDKRB1	AE10387	1	181	R	R	Exon3	Silent	0	AGG	AGA	NP_000701.1	152	538	580	612	644	
Bradykinin Receptor B1	BDKRB1	AE10388	1	296	L	V	Exon3	Missense	0	CTG	CTG	NP_000701.1	181	560	581	613	645	
Bradykinin Receptor B1	BDKRB1	AE10389	2	136	E	E	Exon3	Silent	0	GAG	GAA	NP_000701.1	233	562	582	614	646	
Bradykinin Receptor B2	BDKRB2	AE104810	7	329	R	C	Exon2	Missense	1	GCT	TCT	NP_000814.1	14	564	584	616	648	
Bradykinin Receptor B2	BDKRB2	AE104824	4	918	D	D	Exon3	Silent	1	GAT	GAC	NP_000814.1	311	566	589	621	653	
Bradykinin Receptor B2	BDKRB2	AE104825	4	1046	G	E	Exon3	Missense	1	GCG	GAG	NP_000814.1	354	568	590	622	654	
Angiotensin Converting Enzyme 2	ACE2	AE10867	15	241	N	N	Exon18	Silent	1	AAT	AAC	AAT70220.1	690	843	901	933	965	
Protease inhibitor 4	P14	AE10862	2	526	F	F	Exon2	Silent	0	TTC	TTT	NP_0008061	233	574	603	635	667	
Protease inhibitor 4	P14	AE11056	4	563	S	S	Exon1	Silent	0	AGT	AGC	NP_0008061	199	576	606	639	670	

<210> 1576  
<211> 34  
<212> DNA  
<213> Homo sapiens

<400> 1576  
gcagcagcgg ccgcctgcac agagtgctgc cgac

34

<210> 1577  
<211> 34  
<212> DNA  
<213> Homo sapiens

<400> 1577  
gcagcagtcg acattccgcc agaaaagttg gaag

34

<210> 1578  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 1578  
gcagcagcgg ccgcattggca tcattcctggc cccctctag

39

<210> 1579  
<211> 37  
<212> DNA  
<213> Homo sapiens

<400> 1579  
gcagcagtcg acaaagaagt tggccaattg caggccc

37

Table VII

Table VIIB

Table VIIC

Table VIID

DNA panel	Coriell Catalog #	Sample Description	XPNPEP2	BDKRB1	BDKRB2	TACR1	C1NH	KLK1	PI4	ACE2
HD 100 CAU panel	17255	Caucasian								
HD 100 CAU panel	17256	Caucasian								
HD 100 CAU panel	17257	Caucasian								
HD 100 CAU panel	17258	Caucasian								
HD 100 CAU panel	17259	Caucasian								
HD 100 CAU panel	17260	Caucasian								
HD 100 CAU panel	17261	Caucasian								
HD 100 CAU panel	17262	Caucasian								
HD 100 CAU panel	17263	Caucasian								
HD 100 CAU panel	17264	Caucasian								
HD 100 CAU panel	17265	Caucasian								
HD 100 CAU panel	17266	Caucasian								
HD 100 CAU panel	17267	Caucasian								
HD 100 CAU panel	17268	Caucasian								
HD 100 CAU panel	17269	Caucasian								
HD 100 CAU panel	17270	Caucasian								
HD 100 CAU panel	17271	Caucasian								
HD 100 CAU panel	17272	Caucasian								
HD 100 CAU panel	17273	Caucasian								
HD 100 CAU panel	17274	Caucasian								
HD 100 CAU panel	17275	Caucasian								
HD 100 CAU panel	17276	Caucasian								
HD 100 CAU panel	17277	Caucasian								
HD 100 CAU panel	17278	Caucasian								
HD 100 CAU panel	17279	Caucasian								
HD 100 CAU panel	17280	Caucasian								
HD 100 CAU panel	17281	Caucasian								
HD 100 CAU panel	17282	Caucasian								
HD 100 CAU panel	17283	Caucasian								
HD 100 CAU panel	17284	Caucasian								
HD 100 CAU panel	17285	Caucasian								
HD 100 CAU panel	17286	Caucasian								
HD 100 CAU panel	17287	Caucasian								
HD 100 CAU panel	17288	Caucasian								
HD 100 CAU panel	17289	Caucasian								
HD 100 CAU panel	17290	Caucasian								
HD 100 CAU panel	17291	Caucasian								
HD 100 CAU panel	17292	Caucasian								
HD 100 CAU panel	17293	Caucasian								
HD 100 CAU panel	17294	Caucasian								
HD 100 CAU panel	17295	Caucasian								

Omapatrilat Trial Samples 12 angioedema patients

Table VIII (1 of 2)

Table VIII (2 of 2)

Gene Description	HGNC ID	SNP ID	Exon	RevComp	PCR Amplification Name	Target Name	PCR Left primer (SEQ ID NO:)		PCR Right primer (SEQ ID NO:)	
							PCR Left primer (SEQ ID NO:)	PCR Right primer (SEQ ID NO:)	PCR Left primer (SEQ ID NO:)	PCR Right primer (SEQ ID NO:)
Bradykinin Receptor B1	BDKRB1	AET0595	Exon3	0	AET0595p10	U48231_X2_1a	GGCTCTGATCTGGCTTCCTGTC	T07	CCTGTCCTCTGCTATCCCTGTC	739
Bradykinin Receptor B1	BDKRB1	AET0597	Exon3	0	AET0597p10	U48231_X2_1a	GGCTCTGATCTGGCTTCCTGTC	T08	CCTGTCCTCTGCTATCCCTGTC	740
Bradykinin Receptor B1	BDKRB1	AET0598	Exon3	0	AET0598p10	U48231_X2_1a	GGCTCTGATCTGGCTTCCTGTC	T09	CCTGTCCTCTGCTATCCCTGTC	741
Bradykinin Receptor B1	BDKRB1	AET0599	Exon3	0	AET0599p10	U48231_X2_1a	GGCTCTGATCTGGCTTCCTGTC	T10	AGAAAGGCGAAGCTCTGCA	742
Bradykinin Receptor B2	BDKRB2	AET04518	Exon or Exon	-	AET04518p66	BDKRB2_X3-5a	GGAGGGCAGGAAATTAGCT	710	AGATCGAGACAGAGGAGGG	743
Bradykinin Receptor B2	BDKRB2	AET04519	Exon2	-	AET04519p66	BDKRB2_X3-5a	GGAGGGCAGGAAATTAGCT	711	AGATCGAGACAGAGGAGGG	744
Bradykinin Receptor B2	BDKRB2	AET04520	5' Flank	-	AET04520p66	BDKRB2_X1-3a	CTGGGATTTCCTGCTACCA	713	AGAGCTACGACAGCTGCTACA	745
Bradykinin Receptor B2	BDKRB2	AET04521	5' Flank	-	AET04521p66	BDKRB2_X1-3a	CTGGGATTTCCTGCTACCA	714	AGAGCTACGACAGCTGCTACA	746
Bradykinin Receptor B2	BDKRB2	AET04522	5' Flank	-	AET04522p66	BDKRB2_X1-3a	ACCTTCGGCTCATACCT	715	AGAAACCTCCGGCTCATACCT	747
Bradykinin Receptor B2	BDKRB2	AET04523	5' Flank	-	AET04523p66	BDKRB2_X1-1a	ACGACACGGAAACTCT	716	GAGGGAGTCCTGGCTTC	748
Bradykinin Receptor B2	BDKRB2	AET04524	Exon3	1	AET04524p66	BDKRB2_X3-5a	GGCGAGGCGAGGAAATTAGCT	717	AGATCGAGACAGAGGAGGG	749
Bradykinin Receptor B2	BDKRB2	AET04525	Exon3	1	AET04525p66	BDKRB2_X3-5a	GGCGAGGCGAGGAAATTAGCT	718	AGATCGAGACAGAGGAGGG	750
Bradykinin Receptor B2	BDKRB2	AET04526	Exon3	1	AET04526p66	BDKRB2_X3-4a	GACCTCTCTGGCTTCACTGTA	719	GGCTCTCTGTATTGTTGTTGTA	751
Bradykinin Receptor B2	BDKRB2	AET04527	Exon3	1	AET04527p58	BDKRB2_X3-3a	TOCCAGTTAGCTTGATGAT	720	GGTGTGTTAGCTGATGATGTT	752
Bradykinin Receptor B2	BDKRB2	AET04528	Exon3	1	AET04528p66	BDKRB2_X3-2a	GGGGTATGGCTTAACTAACATT	721	GGGGTATGGCTTAACTAACATT	753
Bradykinin Receptor B2	BDKRB2	AET04529	Exon3	1	AET04529p64	BDKRB2_X3-2a	GGCCACCTCCAAATAAACATT	722	GGGTGATATGGCTACGAGAAAG	754
Angiotensin Converting Enzyme 2	ACE2	AET0981	Intron4	-	AET0981p26	ACE2_X14a	TIAAAACCCAAAGCAAAAGG	723	TTCCTGTTTCAAAAGACCT	755
Angiotensin Converting Enzyme 2	ACE2	AET0982	Intron4	-	AET0982p30	ACE2_X13a	CGCCATAGGAAAGGAAAGGAA	724	GGCCAGTCAGAAAGGAAAGAAC	756
Angiotensin Converting Enzyme 2	ACE2	AET0983	Intron3	-	AET0983p30	ACE2_X13a	CACCATAGGAGAAAGGAAAGGAA	725	GGCCAGTCAGAAAGGAAAGAAC	757
Angiotensin Converting Enzyme 2	ACE2	AET0984	Intron3	-	AET0984p70	ACE2_X3a	GTAAGGTTGGCAGACATCAGG	726	AAAATACTATGTCGAAAGAGA	758
Angiotensin Converting Enzyme 2	ACE2	AET0985	Intron2	-	AET0985p70	ACE2_X3a	GTAAGGTTGGCAGACATCAGG	727	AAAATACTATGTCGAAAGAGA	759
Angiotensin Converting Enzyme 2	ACE2	AET0986	Intron16	-1	AET0986p70	ACE2_X13a	CATATACCTCTGTTGGAAAT	728	GGGTGATATGGCTTGTGTTGC	760
Angiotensin Converting Enzyme 2	ACE2	AET0987	Exon16	1	AET0987p18	ACE2_X14a	TIAAAACCCAAAGCAAAAGG	729	TTCCTGTTTCAAAAGACCT	761
Protease Inhibitor 4	P14	AET1051	Intron1	0	AET1051p26	P14_X22a	GGACATCTGATGAGGAAAGGAA	730	TTGGGGACTCTCTGTTGTTGAA	762
Protease Inhibitor 4	P14	AET1052	Exon2	0	AET1052p26	P14_X22a	GGACATCTGATGAGGAAAGGAA	731	TTGGGGACTCTCTGTTGTTGAA	763
Protease Inhibitor 4	P14	AET1053	Intron2	0	AET1053p26	P14_X22a	GGCTGGGTTACAAAGGAACCT	732	CGCGAGTCCTCTGTTGTTGCT	764
Protease Inhibitor 4	P14	AET1054	Intron2	0	AET1054p26	P14_X22a	GGCTGGGTTACAAAGGAACCT	733	CGCGAGTCCTCTGTTGTTGCT	765
Protease Inhibitor 4	P14	AET1055	Exon1	0	AET1055p18	P14_X15a	AGAGACATCTTCTCCCG	734	CGAGAATTATGGTTGTTGAGG	766
Protease Inhibitor 4	P14	AET1056	5' Flank	0	AET1056p18	P14_X12a	TAGAGCTTCTGGCTTACACA	735	CTAGCTCTGTCACACACTAGA	767
Protease Inhibitor 4	P14	AET1057	5' Flank	0	AET1057p18	P14_X12a	TAGAGCTTCTGGCTTACACA	736	CTAGCTCTGTCACACACTAGA	768
Protease Inhibitor 4	P14	AET1058	5' Flank	0	AET1058p18	P14_X11a	ATGGTGAGCCCGCACTCTA	737	TGTATCCGGTACAGACAGG	769
Protease Inhibitor 4	P14	AET1059	5' Flank	0	AET1059p18	P14_X11a	ATGGTGAGCCCGCACTCTA	738	TGTATCCGGTACAGACAGG	770
Angiotensin Peptidase P (membrane-bound)	XPNPEP2	AET00524	Intron11	0	AET00524p46	XPNPEP2_X12a	TTTCGAAGTCTGGCTACCTG	862	TGCGAGTGTCTGGCTACCTG	988
Angiotensin Peptidase P (membrane-bound)	XPNPEP2	AET00525	Intron13	0	AET00525p50	XPNPEP2_X13a	TAATACTACGGTCTGGCTTG	863	CGCTCTGGCTACCTTCTTCACT	989
Angiotensin Peptidase P (membrane-bound)	XPNPEP2	AET00526	Intron13	0	AET00526p50	XPNPEP2_X13a	TAATACTACGGTCTGGCTTG	864	CGCTCTGGCTACCTTCTTCACT	990
Angiotensin Peptidase P (membrane-bound)	XPNPEP2	AET00527	Intron17	0	AET00527p50	XPNPEP2_X13a	GGGGTCACTTAAATGAGTAC	865	TCAGGGTCACTTAAATGAGTAC	991
Angiotensin Peptidase P (membrane-bound)	XPNPEP2	AET00528	Exon21	0	AET00528p64	XPNPEP2_X22a	GGACITTCACAAAGTGAAGC	866	ACACATACCTCTAACGCCAG	992
Angiotensin Peptidase P (membrane-bound)	XPNPEP2	AET00529	Exon21	0	AET00529p64	XPNPEP2_X22a	GGACITTCACAAAGTGAAGC	867	ACACATACCTCTAACGCCAG	993
Angiotensin Peptidase P (membrane-bound)	XPNPEP2	AET00530	Exon3	0	AET00530p70	XPNPEP2_X5a	GAGAACTCTTCCAGAGGCG	868	TGCACTCTCTGCTACATACCT	994
Bradykinin Receptor B1	BDKRB1	AET0310	Exon3	0	AET0310p26	U48231_X2_1a	ACTICCAAGCTCAAGGAACTC	869	CGTGTTGTTGTTGTTGTTGAA	995
Bradykinin Receptor B1	BDKRB1	AET0311	Exon3	0	AET0311p26	U48231_X2_1a	ACTICCAAGCTCAAGGAACTC	870	CGTGTTGTTGTTGTTGTTGAA	996
Bradykinin Receptor B1	BDKRB1	AET0312	Exon3	0	AET0312p26	U48231_X2_1a	ACTICCAAGCTCAAGGAACTC	871	CGTGTTGTTGTTGTTGTTGAA	997
Bradykinin Receptor B1	BDKRB1	AET0313	Exon3	0	AET0313p26	U48231_X2_1a	ACTICCAAGCTCAAGGAACTC	872	CGTGTTGTTGTTGTTGTTGAA	998
Bradykinin Receptor B1	BDKRB1	AET0314	Exon3	0	AET0314p26	U48231_X2_1a	ACTICCAAGCTCAAGGAACTC	873	CGTGTTGTTGTTGTTGTTGAA	999
Bradykinin Receptor B2	BDKRB2	AET04530	Exon3	0	AET04530p64	BDKRB2_X3-12a	GGCCACCTCTTCAATAAACCT	874	GGGGTATGGCTTAACTAACCT	1000
Bradykinin Receptor B2	BDKRB2	AET04531	Exon3	0	AET04531p62	BDKRB2_X1_1a	ACGACACAGGAAACTCTC	875	GAGGAGCTTCTGGCTACCT	1001
Bradykinin Receptor B2	BDKRB2	AET04532	Exon3	0	AET04532p62	BDKRB2_X1_1a	ACGACACAGGAAACTCTC	876	GAGGAGCTTCTGGCTACCT	1002
Bradykinin Receptor B2	BDKRB2	AET04533	Intron11	-1	AET04533p62	BDKRB2_X1_1a	ACGACACAGGAAACTCTC	877	GAGGAGCTTCTGGCTACCT	1003
Bradykinin Receptor B2	BDKRB2	AET04534	Exon3	-1	AET04534p62	BDKRB2_X3-7a	TCGCTTGTACTCTCTGCTTC	878	TTTGTGTTGTTCTCTGCTTC	1004
Bradykinin Receptor B2	BDKRB2	AET04535	Exon3	-1	AET04535p74	BDKRB2_X3-7a	TCGCTTGTACTCTCTGCTTC	879	TTTGTGTTGTTCTCTGCTTC	1005
Bradykinin Receptor B2	BDKRB2	AET04536	Exon3	-1	AET04536p74	BDKRB2_X3-7a	TCGCTTGTACTCTCTGCTTC	880	TTTGTGTTGTTCTCTGCTTC	1006
Protease Inhibitor 4	P14	AET1054	Exon4	0	AET1054p30	P14_X14a	ATTCTGGCTTGTGTTGTTGTT	881	TGTTACGCCATGACGACAGG	1007
Protease Inhibitor 4	P14	AET1055	Exon1	0	AET1055p12	P14_X11a	ATGGTGAGACCCGACACTCT	882	TGTTACGCCATGACGACAGG	1008
Tachykinin Receptor 1	TACR1	AET0598	Intron3	-1	AET0598p12	TACR1_X3-8a	AAGTCACGACAGGAAACTCTC	883	TGTTACGCCATGACGACAGG	1009
Tachykinin Receptor 1	TACR1	AET0599	Intron3	-1	AET0599p12	TACR1_X3-8a	CTGGGTTTCCACGACACACT	884	TGTTACGCCATGACGACAGG	1010
Angiotensin Converting Enzyme 2	ACE2	AET0980	Intron13	-1	AET0980p30	AEC2_X13a	AEC2_X13a	885	TATGGGTTTCCACGACACACT	1011
Angiotensin Converting Enzyme 2	ACE2	AET0981	Intron13	-1	AET0981p30	AEC2_X13a	AEC2_X13a	886	TATGGGTTTCCACGACACACT	1012

**Table IX (1 of 2)**

Table IX (2 of 2)

GENE DESCRIPTION	HGNC ID	SNP ID	REVCOMP	Target Name	Forward sequencing primer (SEQ ID NO:)	Forward seq name	Reverse sequencing primer (SEQ ID NO:)	Reverse seq name
Bradykinin Receptor 2	BDKRB2	AE10428	Exon3	1	BDKRB2_X3-2a	TTCCTGAGAGACAACTCC	AE104255	TATGCCACACATCTGCC
Bradykinin Receptor 2	BDKRB2	AE10429	Exon3	1	BDKRB2_X3-2a	TTCCTGAGAGACAACTCC	AE104255	TATGCCACACATCTGCC
Angiotensin Converting Enzyme 2	ACE2	AE10981	Imtron14	1	ACE2_x14a	TTTGGAAAGAAAGCACTGGC	AE109827	ATGGATGATCTGGAGAAA
Angiotensin Converting Enzyme 2	ACE2	AE10982	Imtron12	1	ACE2_x13a	CAGCTGTTGACAGAGCTCTCA	AE109831	ACATCTGAAACCTCTAAAG
Angiotensin Converting Enzyme 2	ACE2	AE10983	Imtron13	1	ACE2_x13a	CAGCTGTTGACAGAGCTCTCA	AE109831	ACATCTGAAACCTCTAAAG
Angiotensin Converting Enzyme 2	ACE2	AE10984	Imtron13	1	ACE2_x13a	TGATCTATGCTTCCGCTTCA	AE109871	TCCTGAGAAATTCCATGTT
Angiotensin Converting Enzyme 2	ACE2	AE10985	Imtron2	1	ACE2_x13a	TGATCTATGCTTCCGCTTCA	AE109871	TCCTGAGAAATTCCATGTT
Angiotensin Converting Enzyme 2	ACE2	AE10986	Imtron13	1	ACE2_x13a	CCCTGCTGTTGCTTCA	AE109871	CTCCGCTCTCTCTCTGCTTCA
Angiotensin Converting Enzyme 2	ACE2	AE10987	Imtron13	1	ACE2_x13a	CCCTGCTGTTGCTTCA	AE109871	CTCCGCTCTCTCTCTGCTTCA
Angiotensin Converting Enzyme 2	ACE2	AE10988	Exon16	1	ACE2_x16a	GGCTGGGAAACAACTGAGCA	AE109819	GGCTGGGAAACAACTGAGCA
Protease inhibitor 4	PI4	AE10981	Imtron1	0	PI4_x1a	GATCTGAGAAACATCTGCA	AE110919	GATCTGAGAAACATCTGCA
Protease inhibitor 4	PI4	AE10982	Exon2	0	PI4_x2a	GATCTGAGAAACATCTGCA	AE110923	GATCTGAGAAACATCTGCA
Protease inhibitor 4	PI4	AE10983	Imtron2	0	PI4_x2a	CTTCACATCCATTGAGGG	AE110927	ACTTGGAACTCTCCAGTTT
Protease inhibitor 4	PI4	AE10984	Imtron2	0	PI4_x2a	CTTCACATCCATTGAGGG	AE110927	ACTTGGAACTCTCCAGTTT
Protease inhibitor 4	PI4	AE10985	Exon21	0	PI4_x15a	CTACGCCATCTTCGCTC	AE110919	CGTGTGGATGATTTAGCTA
Protease inhibitor 4	PI4	AE10986	5'Flank	0	PI4_x12a	TGCGGGAGAAAGCTAGAGAT	AE11097	CCACAGACGGAAATGAG
Protease inhibitor 4	PI4	AE10987	5'Flank	0	PI4_x12a	TGCGGGAGAAAGCTAGAGAT	AE11097	CCACAGACGGAAATGAG
Protease inhibitor 4	PI4	AE10988	5'Flank	0	PI4_X11a	AAAGATTAGCTGGTGTGCTT	AE11093	TAATGAACTCTCCAAAGTTG
Amnionopeptidase 1 (membrane-bound)	XPNPEP2	AE10989	Exon11	0	XPNPEP2_x11a	ATTCGATCATCTTGTGAACT	AE109847	GGACAGAACCTCTGACTCT
Amnionopeptidase 1 (membrane-bound)	XPNPEP2	AE10990	Exon12	0	XPNPEP2_x12a	A9TGTAGAGGTGAGGAGCC	AE109851	GGACACTGCTACTGAGACCT
Amnionopeptidase 2 (membrane-bound)	XPNPEP2	AE10991	Exon13	0	XPNPEP2_x13a	A9TGTAGAGGTGAGGAGCC	AE109851	GGACACTGCTACTGAGACCT
Amnionopeptidase 2 (membrane-bound)	XPNPEP2	AE10992	Imtron1	0	XPNPEP2_x13a	AGTGTAGAGGTGAGGAGCC	AE109851	CTTACGCTCTGTTTCTCCAC
Amnionopeptidase 2 (membrane-bound)	XPNPEP2	AE10993	Imtron2	0	XPNPEP2_x13a	AGTGTAGAGGTGAGGAGCC	AE109851	CTTACGCTCTGTTTCTCCAC
Amnionopeptidase 2 (membrane-bound)	XPNPEP2	AE10994	Exon21	0	XPNPEP2_x21_14a	AGGTTCCTTAATCTCCCA	AE10985	CTTACGCTCTGTTTCTCCAC
Amnionopeptidase 2 (membrane-bound)	XPNPEP2	AE10995	Exon21	0	XPNPEP2_x21_14a	AGGTTCCTTAATCTCCCA	AE10985	CTTACGCTCTGTTTCTCCAC
Amnionopeptidase 2 (membrane-bound)	XPNPEP2	AE10996	Exon3	0	XPNPEP2_x3a	ACATCCATGCTTACCTCCCA	AE109819	GGACCTGCTACCTCCCG
Bradykinin Receptor B1	BDKRB1	AE10987	Exon3	0	BDKRB1_X3-2a	CTGAACTCTCTCTCTCTGCA	AE109827	TatGTTATGCTGAACTCTCT
Bradykinin Receptor B1	BDKRB1	AE10988	Exon3	0	BDKRB1_X3-2a	CTGAACTCTCTCTCTCTGCA	AE109827	TatGTTATGCTGAACTCTCT
Bradykinin Receptor B1	BDKRB1	AE10989	Exon3	0	BDKRB1_X3-2a	CTGAACTCTCTCTCTCTGCA	AE109827	TatGTTATGCTGAACTCTCT
Bradykinin Receptor B1	BDKRB1	AE10990	Exon3	0	BDKRB1_X3-2a	CTGAACTCTCTCTCTCTGCA	AE109827	TatGTTATGCTGAACTCTCT
Bradykinin Receptor B2	BDKRB2	AE10991	Exon3	1	BDKRB2_X3-2a	TGCTTGAAGAGACAACTCC	AE109855	TATGCCACACATCTGCC
Bradykinin Receptor B2	BDKRB2	AE10992	Exon3	1	BDKRB2_X3-2a	TGCTTGAAGAGACAACTCC	AE109855	TATGCCACACATCTGCC
Bradykinin Receptor B2	BDKRB2	AE10993	Exon3	1	BDKRB2_X3-2a	TGCTTGAAGAGACAACTCC	AE109855	TATGCCACACATCTGCC
Bradykinin Receptor B2	BDKRB2	AE10994	Exon3	1	BDKRB2_X3-2a	TGCTTGAAGAGACAACTCC	AE109855	TATGCCACACATCTGCC
Protease inhibitor 4	PI4	AE10985	Exon4	0	PI4_x4a	TCTCTGCTCTCTCTGCA	AE110931	CAATGGCTGAACTGCTGAG
Protease inhibitor 4	PI4	AE10986	Exon1	0	PI4_X11a	AAAATTAATGCTTCTGCT	AE11093	TAATGAACTCTCCAAAGTTG
Technidin Receptor 1	TACR1	AE10987	Imtron3	1	TACR1_X4a	TGCTCTCTCTCTCTCTGCA	AE109811	CTTACGCTCTGCTCTCTGCA
Angiotensin Converting Enzyme 2	ACE2	AE10988	Imtron3	1	ACE2_X13a	CAGCTGTTGACAGCTCTCA	AE109815	GTAGCTGCAACCTGAACTG
Angiotensin Converting Enzyme 2	ACE2	AE10989	Imtron3	1	ACE2_X13a	CAGCTGTTGACAGCTCTCA	AE109831	ACATGGCTGAACTGAACTG
Angiotensin Converting Enzyme 2	ACE2	AE10990	Imtron3	1	ACE2_X13a	CAGCTGTTGACAGCTCTCA	AE109831	TCCTCCGCTGCTTCTGAGTT

SNP_ID	ORCHID_LEFT ID (SEQ)	ORCHID_LEFT (SEQ ID No.)	ORCHID_RIGHT (SEQ ID No.)	ORCHID_RIGHT (SEQ ID No.)	ORCHID_SNPsIT (SEQ ID No.)	
AE100s1	TATCATTTGTGCCCTATGACCG	1066	CAGGAGGAGAGGG	1154	CCTCATCGATGCTGCTGCTGCTGCTC	1242
AE100s10	AACTCTCATCATCAGGTACCAAAG	1067	CGGACATTTGATTCAGACTCC	1155	GTGGTTTCCAAACCTTATGATGAC	1243
AE100s11	ATAGAATGACTTCCCTACGAGGA	1068	CAGCTTAACCCCTGACTGCG	1156	TGGAGCCCAAGCCCCAGAGGT	1244
AE100s12	TCCAGAGGGACTGCCTG	1069	GAAGGCCAGCTTACCCCTG	1157	ACCCAGGCCAGAGGTCTCC	1245
AE100s13	ATAGAATGACTTCCCTACGAGGA	1070	GTGAGAAAGGGAGGATGTT	1158	ATGTTGAGAAGCTGAGCTAACCTG	1246
AE100s14	N/A	N/A	N/A	N/A	N/A	N/A
AE100s15	ACCCCTCTGTCCTCGAG	1071	GATCGAGGACAAACGGAG	1159	CCGGSCTCTCCCTCANGCTTCT	1247
AE100s16	AAGCAAGGAAAGGAAAGGAA	1072	GTGAGGAAATAGAAGAGGGTATAGG	1160	AGAAAAGCTGNCCTGAGATCAG	1248
AE100s17	N/A	N/A	N/A	N/A	N/A	N/A
AE100s18	AACACACAGACCCCTCTCA	1073	GATCCAGAGCATCTATGAGC	1161	TACCTTAATTAATAATAAACCCAG	1249
AE100s19	N/A	N/A	N/A	N/A	N/A	N/A
AE100s2	ATAGAATGACTTCCCTACGAGGA	1074	GATCTTGTGCACTCACTCCC	1162	CGAACAGATCTCCTTTCAGAACATC	1250
AE100s20	TTACCAACAGGAGGAGGAGG	1075	GATTCGGTACTGGAGCTCG	1163	AGACTTCACCTCTGGCANCCTGGCT	1251
AE100s21	N/A	N/A	N/A	N/A	N/A	N/A
AE100s22	N/A	N/A	N/A	N/A	N/A	N/A
AE100s23	TTTGCCTAAGGACACACAAATT	1076	GAGTGGGCTCAAGGAACT	1164	CTGGATGTTGCTTAAAGGTTGAA	1252
AE100s24	CGCTATCTGATCTCATCATCT	1077	CGAACCTGGAGTTGG	1165	TTCGACCTCTGGTNTAACAGACCT	1253
AE100s25	N/A	N/A	N/A	N/A	N/A	N/A
AE100s26	N/A	N/A	N/A	N/A	N/A	N/A
AE100s27	ACAAAGTAAAGCTGTGAGGAAGG	1078	GAGGCCAAAAAGTTAACTGA	1166	TTCACCTTGGCTGACCTTCCAGGAAC	1254
AE100s28	N/A	N/A	N/A	N/A	N/A	N/A
AE100s29	N/A	N/A	N/A	N/A	N/A	N/A
AE100s3	N/A	N/A	N/A	N/A	N/A	N/A
AE100s30	TATCTTCTCTGAGTGGCACCA	1079	CAATGAGAAGGAAACGGG	1167	TCACCTGGCTCCCTACGGAGATTC	1255
AE100s4	TCCCTGCTGCTTCCCCGG	1080	AATATTGTCGACTGATTACCGAATAG	1168	TATTCAAGCAGTACAGCAGGCTCAG	1256
AE100s5	N/A	N/A	N/A	N/A	N/A	N/A
AE100s6	TGTGTGTGATGATGTTGAGGTG	1081	CTTGTGCACTTCCATACCTGCAA	1169	ACCTCTCATGAGGCTATAAAG	1257
AE100s7	ATTCAGAATGATGCAAAAGCCAG	1082	GTCAGCTCTGGTAACTGTTTG	1170	AGAGATTTCTTCTGAAAGGTTT	1258
AE100s8	GGAAATCTCACTGTGCTG	1083	CAAGTCGGCGCAACAGTA	1171	GTAAGGAGGTCTGTTGACAGGG	1259
AE100s9	AAACATGAGAAGGAGAAACACAC	1084	TTTCGAGGACATGGCAAG	1172	CAAGAGTAGAGAAATGGCAAGAA	1260
AE101s1	AACTTGTGCTCTACAACTACGCT	1085	GATGAGATAATTGGAGAAACCTTGTAG	1173	CGAGTAATTGTCCTTGGGGCC	1261
AE101s10	N/A	N/A	N/A	N/A	N/A	N/A
AE103s11	TGGACTTGATGATGTTGACCAATT	1086	GACTCTGACCTCTGCTC	1174	ATCCCTGAATTTATCTGCCCCCT	1262
AE103s12	N/A	N/A	N/A	N/A	N/A	N/A
AE103s13	CCACCCAGGTTCTGGTATTG	1087	CTTGTGATGAGCAAAATGGATTTAGA	1175	CGCGAGGAGAACATAACATTC	1263
AE103s14	TGTCTGGCGAGAGATACTGGA	1088	CTTGGAGTTAGCTTAAGAAGC	1176	ACAGATATCTGTTATGCTCTCTTA	1264
AE103s15	N/A	N/A	N/A	N/A	N/A	N/A
AE103s16	TGACAAATGCTCAGAGGCC	1089	CAACGGGCAAAAGGTCC	1177	CTGGGACCTCTGCTGAGACGTCG	1265
AE103s17	N/A	N/A	N/A	N/A	N/A	N/A
AE103s18	ATTCGAAACATCCGGCT	1090	ACCCCTCAATCTGCGA	1178	TGAACTTAACTGGCTTCTTATC	1266
AE103s19	N/A	N/A	N/A	N/A	N/A	N/A
AE103s20	N/A	N/A	N/A	N/A	N/A	N/A
AE103s21	N/A	N/A	N/A	N/A	N/A	N/A
AE103s22	N/A	N/A	N/A	N/A	N/A	N/A
AE103s23	N/A	N/A	N/A	N/A	N/A	N/A
AE103s24	N/A	N/A	N/A	N/A	N/A	N/A
AE103s25	N/A	N/A	N/A	N/A	N/A	N/A
AE103s26	N/A	N/A	N/A	N/A	N/A	N/A
AE103s27	N/A	N/A	N/A	N/A	N/A	N/A
AE103s28	N/A	N/A	N/A	N/A	N/A	N/A
AE103s29	N/A	N/A	N/A	N/A	N/A	N/A
AE103s30	N/A	N/A	N/A	N/A	N/A	N/A
AE104s1	N/A	N/A	N/A	N/A	N/A	N/A
AE104s10	GTTTGGGGCTCTAGGGTGC	1094	GTGGGATGAGAGGTGAGGAC	1182	GTGGGATGAGAGGTGAGGACCA	1270

BNP_ID	ORCHID_LEFT ID No.1	ORCHID_LEFT (SEQ ID No.1)	ORCHID_RIGHT (SEQ ID No.1)	ORCHID_RIGHT (SEQ ID No.1)	ORCHID_SNP1 ID No.1	
AE104s11	TTCGATGTTGAAATGCTTCCTG	1095	GGCTCTGATGCTGGTGTAGT	1183	TGACACATAGCAGCATTTGAGTT	1271
AE104s12	ATTTTCCTGTTGGATGTAATG	1096	CGGCCCTATGCTGGTGTAGT	1184	TAACAGCTCATGTCAGTCAGC	1272
AE104s13	GGCATATGGGAGGAGCTC	1097	AAAAAAAGGGCTTGTGTTCA	1185	GGGCACTCATGCAACCAAGGCAC	1273
AE104s14	AAGCTAACTGAGCTGCGCCCT	1098	AAGGGGGCCCAATATAGTC	1186	CCCTAGAGAGCTGAAAGGAAATG	1274
AE104s16	GATCCATGATGATGGAGGG	1099	CACTGATGGAAATTCATATATCC	1187	ATTCTTCACTATANTATNAACAAA	1275
AE104s17	GATGAAACAGATGAAAGAGG	1100	CATAAACTCCCTCCCTCAT	1188	TACGTTGAGCTGGATGAGCCCAAGGTT	1276
AE104s18	AGAAAGAAAGATGGTATGATGCA	1101	CAATTGAGTCAGGGACTCAGCA	1189	ACAGGGCTGGAGATTCGCAAAATAGAC	1277
AE104s19	TAACATGTGAACTGAGATCCCTT	1102	CACTCTAGTCGCAATATGTCCTC	1190	GTGGTCGGACGGAGCTCTCAC	1278
AE104s2	GGAGGCAATAATGTCGTTTTGATAA	1103	CTTCACCTGTCGTCGTCCTG	1191	GTCAAGGGGGCNACCTGGCGGG	1279
AE104s20	TTTACACCTCCCAGGGCTGTAG	1104	CTTCCTCCCAGATCCCTCTGG	1192	TTTTGAGAGCTTAACCCCTTCCTTC	1280
AE104s21	GGATTTCCTTGTGATGCCAGTAC	1105	CATACTCTCGAGAAACGG	1193	GCAGAGCTGTGTCGTTCTGGGT	1281
AE104s22	N/A	N/A	N/A	N/A	N/A	N/A
AE104s23	AGAGCTGGAGTCGGCGGG	1106	GGAGAGTCGAGACCTCAG	1194	GAAGGCCCCAGGGCTGAGACATCA	1282
AE104s24	N/A	N/A	N/A	N/A	N/A	N/A
AE104s25	N/A	N/A	N/A	N/A	N/A	N/A
AE104s26	TGAAATGATTAAGAAACCCAGG	1107	GTTCCTCCCTCCCTGCC	1195	CATTTCACCAAAACCTGGATGCG	1283
AE104s27	TGGACCCCTCTGTCGAAC	1108	GAAGAGAAGGGAGCACTCTCA	1196	GCTTGTGGTACAGTCGCCAGTC	1284
AE104s28	N/A	N/A	N/A	N/A	N/A	N/A
AE104s29	N/A	N/A	N/A	N/A	N/A	N/A
AE104s3	TTCGCAAGGGAGGAATC	1109	CAACCCCTGCACTCCAGC	1197	GAGGAAAGGGCTGGAGCTGAGTCATCG	1285
AE104s30	N/A	N/A	N/A	N/A	N/A	N/A
AE104s31	N/A	N/A	N/A	N/A	N/A	N/A
AE104s32	N/A	N/A	N/A	N/A	N/A	N/A
AE104s33	TAGGGATACAACTGGCTAGGCT	1110	GTTCGGGACCCCATTTCTAT	1198	ACCTTTGTTGATGTTTCACTGTA	1286
AE104s34	ACGACTGGTGTCTACACCG	1111	GTACATGTGAGGCATCTTACGC	1199	GGCTCCCCAAATCTGATCTGCTCCA	1287
AE104s35	N/A	N/A	N/A	N/A	N/A	N/A
AE104s36	CCCTCTCTGTCATATCA	1112	CATCTGAGGAACCTAAAGCTCA	1200	ACCAAGACCCCCCTGACCGTC	1288
AE104s4	AGTGAAGGGCTTGAGTGCA	1113	CTTGGATGAAAGAAAGGAGGCA	1201	ACGGTTGCGAGGAGACAGCTGGATGAGG	1289
AE104s5	TGGAGGGTTGAGGAGCA	1114	CAAGAGAGGGCTCTTGTAT	1202	GGTGGATGAGGCTGGCTGCTGCT	1290
AE104s6	GGCTCACAACTGGTGAATCTC	1115	CAAGAGACCCCTGGCGGA	1203	GTTCCTCTGGAGAAAGACTCTGG	1291
AE104s7	ACACTGGTGTCTACACCG	1116	AACCCCTTACCCACACGC	1204	CCCTCTCTCCAAGCTTGTCCCACAA	1292
AE104s8	ATGAACTGGACCCCTGGTT	1117	GGGAGCCAGGGTTCAGCTC	1205	GAAGGGAGACAGCTGGAGGAG	1293
AE104s9	TATTTCTAAGCTCACTGCTTCTCTTAAAG	1118	GAAGCTGGTGGAGGGTAAAGG	1206	AGGGTGGTGTGAGCTGTTGAGCTTC	1294
AE104s10	GGAGGAGCTGCTGGGGG	1119	AGGTGTTTCACTCCCTCTGGCA	1207	CCCGCCGCTGGAGAAAGAACGACA	1295
AE104s11	ATTCGAGACAGATGGGG	1120	CAAACCTGAGATGGGGAGAC	1208	GAAGAGGCGCTTGGAGACTGTAG	1296
AE104s12	N/A	N/A	N/A	N/A	N/A	N/A
AE104s13	GGAGGGAAAGCTCGCAA	1121	TTCAGTTGGTGTGGCCAA	1209	AACTCTGAAACCTGAGATGGGTCA	1297
AE104s14	TGTGGGGGAGCTTGTGG	1122	GATGCTGAATGGGGAAAGG	1210	AGGCTTACACCGCTCTCTGAG	1298
AE104s15	ATTCCTGTCGGCCGAC	1123	CATACTCTCCCCATAGAC	1211	CGAACCTGTTCTCTGGTCCCCAGAGCA	1299
AE104s16	TATCAAAGGCCACGCG	1124	CACAAAGAAATGGTACAGCC	1212	TACGGCGAGAGAGGGCATGGCG	1300
AE104s17	ATGGCTCTGCTGTTGAGTGTGC	1125	CATCATACATCCCTCTAGC	1213	CCAGCAGGAGGAGCCACCCCA	1301
AE104s18	ATACCTGGGGATATTGTGCG	1126	CTACCAAGGAGCAAGTCTCTG	1214	CCAAAGGAGAGGAGGAGGGG	1302
AE104s19	TGCAAGATTCATCTGAAATA	1127	CIGGTTGAGCTAAACAAATCT	1215	AGCTGGACCCACCTTTCACAA	1303
AE104s20	AAAGCTGGTGGAGCTTGTAA	1128	TCAAAATTCATCTCTCCCTCT	1216	TCCCTATCTGTCACCTTCAGCTTC	1304
AE104s21	TGTTAGCTAACAGATGAGG	1129	CATGAAATTCCCTCTATCTG	1217	ACCATCATCTGACCCCTTGTGAGTC	1305
AE104s22	ATGGCTCTGAGGAGCTGCG	1130	CCCGAGGAGGAGGGAG	1218	AGGAGCTTGGAGGAGGAGGAG	1306

TABLE X (3 of 3)

SNP_ID	ORCHID_LEFT	ORCHID_RIGHT	ORCHID_SEQ (SEQ ID NO.)		ORCHID_SNIP_ID	ORCHID_SNIPIT (SEQ ID NO.)
			SEQ ID NO.1	SEQ ID NO.2		
AB10s8	N/A	N/A	N/A	N/A	N/A	N/A
AB10s9	N/A	N/A	N/A	N/A	N/A	N/A
AE107s1	GTTGCTGACTCTGCAATTGCGAATGATC	1131	ACACACAGGATGAGCTGCTGAC	1219	CAAATGCTGCTAAATGATGAGATGCC	1307
AE107s2	AGCATCGAACCGAGAAATGGTATGATG	1132	CTTCCTGCGCCCTTTCCTC	1220	TCCCTTENACAGGAGTCCCATCTCC	1308
AE107s3	CCTGCTGTATACCATCAGCATG	1133	CATACAAATTCCTGTTGATGTC	1221	GCTGTGAGTGTGCGGGATGCGCCACC	1309
AE107s4	ATGACACCGAGAAATGGTATGTCG	1134	GGGAGAAAGAGGCTGCA	1222	AAGCCTGGATGGAGAACCTCTGCA	1310
AE107s5	ACCTGAGCAGCTGGCT	1135	CCCTGCGACCCAGCTGG	1223	TCAGCCGACCCAGCTGG	1311
AE107s6	CCATGAAATCAATGTCATCC	1136	CAGCTCTGCGCCAGTCG	1224	ATCTGCTACGTTGCTCATCACC	1312
AE109s1	ATATGGTTATTCATTAAGGATGGTACATT	1137	GAATTGAGTATTGTCAGTCAGTC	1225	ATCTGGAACTATAGTTGAAAGAA	1313
AE109s2	GGGGTTCAAGGSCCTTT	1138	GCAAAATTGACCAATGCAAGAGA	1226	GAGGGTCCAGANSTAAATATATTA	1314
AE109s3	TGGGGCAAAAGGAGACTAG	1139	GCTGAAAGAACAGAAACAGAATTTC	1227	AAGTACACAGGAAATGGTGTGAA	1315
AE109s4	GTGTGAAACACACATATTCGAAAT	1140	TGGAAAGTTGTAACCCGATTAATC	1228	TCTATAACAGTTAAATTAGTGGC	1316
AE109s5	GTGTGCAACTGAAATTAAGATAATAACAA	1141	ACATGCCAACAGAAATGAAATCG	1229	GAATTTGTCGAAGAATGCTTA	1317
AE109s6	AACTCAAAACGAAATTTCCCTG	1142	GTTCACCAAATACACACAAATPACAGPATT	1230	CACATCTTAATGACTCAGATAATG	1318
AE109s7	CCCTCACCCCTAGGAAAGTAAAA	1143	TTCGAAACCAACGAAATTCCTTTAATT	1231	TTCAGTTCTGAAATTTACGACAC	1319
AE109s8	N/A	N/A	N/A	N/A	N/A	N/A
AE109s9	AGGCTCACTAAAGGAAATT	1144	TGCCCTCCCTGCTGTTATG	1232	CTTGTTGAAAGCCCTAAATTCCTTC	1320
AE110s1	N/A	N/A	N/A	N/A	N/A	N/A
AE110s10	CACCTTGACTGGTGTGAG	1145	ATGGCCGATTGCTG	1233	GENTGGCACCAGAGTGGAGCAGCCAC	1321
AE110s11	CACCTCTGCAACATCTCA	1146	CATGGTGCTATCAGGAAATTG	1234	AACCTTCGCGENCATGGCTGGAAACA	1322
AE110s12	AGATTGGGGAGAAATCTG	1147	CAGTAAACTGGCTTGTAAATGTTAC	1235	TATCTTGACAGATGTTTATGAA	1323
AE110s2	CTGTAACCTCTTTCACCTTCCTT	1148	CCAGCATCATGGCACCC	1236	CCGAGCTGTTGCTGTCATCAACATA	1324
AE110s3	AAGGAAGGCTCTGCCAG	1149	GATGCCAACTCTGTTCTGTTAAATT	1237	GATCTGCGCTCTGTCANTANTCTPATG	1325
AE110s4	N/A	N/A	N/A	N/A	N/A	N/A
AE110s5	CTTATCAAGAACCTGCAAGAA	1150	GATTAGGATATACCAATGATGTC	1238	GAGGGGAGATGTTGCTATGGTCAG	1326
AE110s6	GTCAAAATTAATGGTAAAGTGG	1151	TTTCGATGAGTGTGTTGTTGATGTC	1239	AGACCTAAATAAAACCTGAGGAT	1327
AE110s7	AGGGTCAAACTAAATGGCTGAA	1152	CACTGCTCTTGTGTTGACTGTTTC	1240	TAACACCATATAAGGACTCTCACGAG	1328
AE110s8	AGAAAATGGTATTCCTTCAGGA	1153	CTGTAAGGGCTCAAGAATGCTCTTG	1241	TATGAACTGGCTTACGTTCTATCCTCC	1329
AE110s9	N/A	N/A	N/A	N/A	N/A	N/A

SNP_ID	GBS_LEFT	GBS_RIGHT	GBS_LEFT (SEQ ID NO:)	GBS_RIGHT	GBS_RIGHT (SEQ ID NO:)
AE100s1	TGTAAGAACGACGGCCAGTGGTCTCCCTCCACT	1330	CAGGAAACGCTTATGACCAAGACCTCTGGGTC	1451	
AE100s10	TGTAAAAGACGGCCAGTGGTCACTACAGGTGATCT	1331	CAGGAAACGCTTATGACCAAGACCTCTGGGTC	1452	
AE100s11	TGTAAGAACGACGGCCAGTGGTCACTACAGGTGATCT	1332	CAGGAAACGCTTATGACCAAGACCTCTGGGTC	1453	
AE100s12	TGTAAAAGACGGCCAGTGGTCACTACAGGTGATCT	1333	CAGGAAACGCTTATGACCAAGACCTCTGGGTC	1454	
AE100s13	TGTAAAAGACGGCCAGTGGTCACTACAGGTGATCT	1334	CAGGAAACGCTTATGACCAAGACCTCTGGGTC	1455	
AE100s14	TGTAAAAGACGGCCAGTGGTCACTACAGGTGATCT	1335	CAGGAAACGCTTATGACCAAGACCTCTGGGTC	1456	
AE100s15	TGTAAAAGACGGCCAGTGGTCACTACAGGTGATCT	1336	CAGGAAACGCTTATGACCAAGACCTCTGGGTC	1457	
AE100s16	TGTAAAAGACGGCCAGTGGTCACTACAGGTGATCT	1337	CAGGAAACGCTTATGACCAAGACCTCTGGGTC	1458	
AE100s17	TGTAAAAGACGGCCAGTGGTCACTACAGGTGATCT	1338	CAGGAAACGCTTATGACCAAGACCTCTGGGTC	1459	
AE100s18	TGTAAAAGACGGCCAGTGGTCACTACAGGTGATCT	1339	CAGGAAACGCTTATGACCAAGACCTCTGGGTC	1460	
AE100s19	TGTAAAAGACGGCCAGTGGTCACTACAGGTGATCT	1340	CAGGAAACGCTTATGACCAAGACCTCTGGGTC	1461	
AE100s2	TGTAAGAACGACGGCCAGTGGTCACTACAGGTGATCT	1341	CAGGAAACGCTTATGACCAAGACCTCTGGGTC	1462	
AE100s20	TGTAAGAACGACGGCCAGTGGTCACTACAGGTGATCT	1342	CAGGAAACGCTTATGACCAAGACCTCTGGGTC	1463	
AE100s21	TGTAAGAACGACGGCCAGTGGTCACTACAGGTGATCT	1343	CAGGAAACGCTTATGACCAAGACCTCTGGGTC	1464	
AE100s22	TGTAAGAACGACGGCCAGTGGTCACTACAGGTGATCT	1344	CAGGAAACGCTTATGACCAAGACCTCTGGGTC	1465	
AE100s23	TGTAAGAACGACGGCCAGTGGTCACTACAGGTGATCT	1345	CAGGAAACGCTTATGACCAAGACCTCTGGGTC	1466	
AE100s24	TGTAAGAACGACGGCCAGTGGTCACTACAGGTGATCT	1346	CAGGAAACGCTTATGACCAAGACCTCTGGGTC	1467	
AE100s25	TGTAAGAACGACGGCCAGTGGTCACTACAGGTGATCT	1347	CAGGAAACGCTTATGACCAAGACCTCTGGGTC	1468	
AE100s26	TGTAAGAACGACGGCCAGTGGTCACTACAGGTGATCT	1348	CAGGAAACGCTTATGACCAAGACCTCTGGGTC	1469	
AE100s27	TGTAAGAACGACGGCCAGTGGTCACTACAGGTGATCT	1349	CAGGAAACGCTTATGACCAAGACCTCTGGGTC	1470	
AE100s28	TGTAAGAACGACGGCCAGTGGTCACTACAGGTGATCT	1350	CAGGAAACGCTTATGACCAAGACCTCTGGGTC	1471	
AE100s29	TGTAAGAACGACGGCCAGTGGTCACTACAGGTGATCT	1351	CAGGAAACGCTTATGACCAAGACCTCTGGGTC	1472	
AE100s3	TGTAAGAACGACGGCCAGTGGTCACTACAGGTGATCT	1352	CAGGAAACGCTTATGACCAAGACCTCTGGGTC	1473	
AE100s30	TGTAAGAACGACGGCCAGTGGTCACTACAGGTGATCT	1353	CAGGAAACGCTTATGACCAAGACCTCTGGGTC	1474	
AE100s4	TGTAAGAACGACGGCCAGTGGTCACTACAGGTGATCT	1354	CAGGAAACGCTTATGACCAAGACCTCTGGGTC	1475	
AE100s5	TGTAAGAACGACGGCCAGTGGTCACTACAGGTGATCT	1355	CAGGAAACGCTTATGACCAAGACCTCTGGGTC	1476	
AE100s6	TGTAAGAACGACGGCCAGTGGTCACTACAGGTGATCT	1356	CAGGAAACGCTTATGACCAAGACCTCTGGGTC	1477	
AE100s7	TGTAAGAACGACGGCCAGTGGTCACTACAGGTGATCT	1357	CAGGAAACGCTTATGACCAAGACCTCTGGGTC	1478	
AE100s8	TGTAAGAACGACGGCCAGTGGTCACTACAGGTGATCT	1358	CAGGAAACGCTTATGACCAAGACCTCTGGGTC	1479	
AE100s9	TGTAAGAACGACGGCCAGTGGTCACTACAGGTGATCT	1359	CAGGAAACGCTTATGACCAAGACCTCTGGGTC	1480	
AE100s10	TGTAAGAACGACGGCCAGTGGTCACTACAGGTGATCT	1360	CAGGAAACGCTTATGACCAAGACCTCTGGGTC	1481	
AE100s11	TGTAAGAACGACGGCCAGTGGTCACTACAGGTGATCT	1361	CAGGAAACGCTTATGACCAAGACCTCTGGGTC	1482	
AE100s12	TGTAAGAACGACGGCCAGTGGTCACTACAGGTGATCT	1362	CAGGAAACGCTTATGACCAAGACCTCTGGGTC	1483	
AE100s13	TGTAAGAACGACGGCCAGTGGTCACTACAGGTGATCT	1363	CAGGAAACGCTTATGACCAAGACCTCTGGGTC	1484	
AE100s14	TGTAAGAACGACGGCCAGTGGTCACTACAGGTGATCT	1364	CAGGAAACGCTTATGACCAAGACCTCTGGGTC	1485	
AE100s15	TGTAAGAACGACGGCCAGTGGTCACTACAGGTGATCT	1365	CAGGAAACGCTTATGACCAAGACCTCTGGGTC	1486	
AE100s16	TGTAAGAACGACGGCCAGTGGTCACTACAGGTGATCT	1366	CAGGAAACGCTTATGACCAAGACCTCTGGGTC	1487	
AE100s17	TGTAAGAACGACGGCCAGTGGTCACTACAGGTGATCT	1367	CAGGAAACGCTTATGACCAAGACCTCTGGGTC	1488	
AE100s18	TGTAAGAACGACGGCCAGTGGTCACTACAGGTGATCT	1368	CAGGAAACGCTTATGACCAAGACCTCTGGGTC	1489	
AE100s19	TGTAAGAACGACGGCCAGTGGTCACTACAGGTGATCT	1369	CAGGAAACGCTTATGACCAAGACCTCTGGGTC	1490	
AE100s20	TGTAAGAACGACGGCCAGTGGTCACTACAGGTGATCT	1370	CAGGAAACGCTTATGACCAAGACCTCTGGGTC	1491	
AE100s21	TGTAAGAACGACGGCCAGTGGTCACTACAGGTGATCT	1371	CAGGAAACGCTTATGACCAAGACCTCTGGGTC	1492	
AE100s22	TGTAAGAACGACGGCCAGTGGTCACTACAGGTGATCT	1372	CAGGAAACGCTTATGACCAAGACCTCTGGGTC	1493	
AE100s23	TGTAAGAACGACGGCCAGTGGTCACTACAGGTGATCT	1373	CAGGAAACGCTTATGACCAAGACCTCTGGGTC	1494	
AE100s24	TGTAAGAACGACGGCCAGTGGTCACTACAGGTGATCT	1374	CAGGAAACGCTTATGACCAAGACCTCTGGGTC	1495	
AE100s25	TGTAAGAACGACGGCCAGTGGTCACTACAGGTGATCT	1375	CAGGAAACGCTTATGACCAAGACCTCTGGGTC	1496	

AE104511	TGTAACACGACGGCCAGTCGGCACTTGACAAATCT	1376	CGGAAACAGCTATGACCGCCATGTGTTTCA	1497
AE104512	TGTAACACGACGGCCAGTCGGCACTTGACAAATCTCA	1377	CGGAAACAGCTATGACCGCCAGTCGGTTTCA	1498
AE104513	TGTAACACGACGGCCAGTCGGCACTTGACAAATCTCA	1378	CGGAAACAGCTATGACCGCAAGAAACG	1499
AE104514	TGTAACACGACGGCCAGTCGGCACTTGACAAATCTAGGCC	1379	CGGAAACAGCTATGACCGCAATTCGTTG	1500
AE104515	TGTAACACGACGGCCAGTCGGCACTTGACAAATCTGACCC	1380	CGGAAACAGCTATGACCGCAATTCGTTG	1501
AE104516	TGTAACACGACGGCCAGTCGGCACTTGACAAATCTTAA	1381	CGGAAACAGCTATGACCGCACTGTTCTACT	1502
AE104517	TGTAACACGACGGCCAGTCGGCACTTGACAAATCTTAA	1382	CGGAAACAGCTATGACCGCACTGTTCTCG	1503
AE104518	TGTAACACGACGGCCAGTCGGCACTTGACAAATCTTCA	1383	CGGAAACAGCTATGACCGCACTTCTGATG	1504
AE104519	TGTAACACGACGGCCAGTCGGCACTTGACAAATCTTCC	1384	CGGAAACAGCTATGACCGCACTTCTGACCAACG	1505
AE104520	TGTAACACGACGGCCAGTCGGCACTTGACAAATCTTCA	1385	CGGAAACAGCTATGACCGCACTTCTGAT	1506
AE104521	TGTAACACGACGGCCAGTCGGCACTTGACAAATCTGCG	1386	CGGAAACAGCTATGACCGCACTTCTGAGTC	1507
AE104522	TGTAACACGACGGCCAGTCGGCACTTGACAAATCTTAA	1387	CGGAAACAGCTATGACCGCACTTCTGAGAA	1508
AE104523	TGTAACACGACGGCCAGTCGGCACTTGACAAATCTTCA	1388	CGGAAACAGCTATGACCGCACTTCTGCA	1509
AE104524	TGTAACACGACGGCCAGTCGGCACTTGACAAATCTTCA	1389	CGGAAACAGCTATGACCGCACTTCTGAGTC	1510
AE104525	TGTAACACGACGGCCAGTCGGCACTTGACAAATCTTCA	1390	CGGAAACAGCTATGACCGCACTTCTGAGTC	1511
AE104526	TGTAACACGACGGCCAGTCGGCACTTGACAAATCTGAGTA	1391	CGGAAACAGCTATGACCGCACTTCTGAGTC	1512
AE104527	TGTAACACGACGGCCAGTCGGCACTTGACAAATCTGATG	1392	CGGAAACAGCTATGACCGCACTTCTGAGCAAGCA	1513
AE104528	TGTAACACGACGGCCAGTCGGCACTTGACAAATCTGCTG	1393	CGGAAACAGCTATGACCGCACTTCTGAGCAAGCA	1514
AE104529	TGTAACACGACGGCCAGTCGGCACTTGACAAATCTGCTTC	1394	CGGAAACAGCTATGACCGCACTTCTGAGCACTG	1515
AE104530	TGTAACACGACGGCCAGTCGGCACTTGACAAATCTGCTTC	1395	CGGAAACAGCTATGACCGCACTTCTGAGCAAGCA	1516
AE104531	TGTAACACGACGGCCAGTCGGCACTTGACAAATCTGCTTC	1396	CGGAAACAGCTATGACCGCACTTCTGAGCAAGCA	1517
AE104532	TGTAACACGACGGCCAGTCGGCACTTGACAAATCTGCTTC	1397	CGGAAACAGCTATGACCGCACTTCTGAGCACTG	1518
AE104533	TGTAACACGACGGCCAGTCGGCACTTGACAAATCTGCTTC	1398	CGGAAACAGCTATGACCGCACTTCTGAGCAACCA	1519
AE104534	TGTAACACGACGGCCAGTCGGCACTTGACAAATCTGCTTC	1399	CGGAAACAGCTATGACCGCACTTCTGAGCAACCA	1520
AE104535	TGTAACACGACGGCCAGTCGGCACTTGACAAATCTGCTTC	1400	CGGAAACAGCTATGACCGCACTTCTGAGCAACCACTG	1521
AE104536	TGTAACACGACGGCCAGTCGGCACTTGACAAATCTGCTTC	1401	CGGAAACAGCTATGACCGCACTTCTGAGCAACCACTG	1522
AE104537	TGTAACACGACGGCCAGTCGGCACTTGACAAATCTGCTTC	1402	CGGAAACAGCTATGACCGCACTTCTGAGCAACCA	1523
AE104538	TGTAACACGACGGCCAGTCGGCACTTGACAAATCTGCTTC	1403	CGGAAACAGCTATGACCGCACTTCTGAGCAACCA	1524
AE104539	TGTAACACGACGGCCAGTCGGCACTTGACAAATCTGCTTC	1404	CGGAAACAGCTATGACCGCACTTCTGAGCAACCTG	1525
AE104540	TGTAACACGACGGCCAGTCGGCACTTGACAAATCTGCTTC	1405	CGGAAACAGCTATGACCGCACTTCTGAGCAACCTG	1526
AE104541	TGTAACACGACGGCCAGTCGGCACTTGACAAATCTGCTTC	1406	CGGAAACAGCTATGACCGCACTTCTGAGCAACCTG	1527
AE104542	TGTAACACGACGGCCAGTCGGCACTTGACAAATCTGCTTC	1407	CGGAAACAGCTATGACCGCACTTCTGAGCAACCTG	1528
AE104543	TGTAACACGACGGCCAGTCGGCACTTGACAAATCTGCTTC	1408	CGGAAACAGCTATGACCGCACTTCTGAGCAACCTG	1529
AE104544	TGTAACACGACGGCCAGTCGGCACTTGACAAATCTGCTTC	1409	CGGAAACAGCTATGACCGCACTTCTGAGCAACCTG	1530
AE104545	TGTAACACGACGGCCAGTCGGCACTTGACAAATCTGCTTC	1410	CGGAAACAGCTATGACCGCACTTCTGAGCAACCTG	1531
AE104546	TGTAACACGACGGCCAGTCGGCACTTGACAAATCTGCTTC	1411	CGGAAACAGCTATGACCGCACTTCTGAGCAACCTG	1532
AE104547	TGTAACACGACGGCCAGTCGGCACTTGACAAATCTGCTTC	1412	CGGAAACAGCTATGACCGCACTTCTGAGCAACCTG	1533
AE104548	TGTAACACGACGGCCAGTCGGCACTTGACAAATCTGCTTC	1413	CGGAAACAGCTATGACCGCACTTCTGAGCAACCTG	1534
AE104549	TGTAACACGACGGCCAGTCGGCACTTGACAAATCTGCTTC	1414	CGGAAACAGCTATGACCGCACTTCTGAGCAACCTG	1535
AE104550	TGTAACACGACGGCCAGTCGGCACTTGACAAATCTGCTTC	1415	CGGAAACAGCTATGACCGCACTTCTGAGCAACCTG	1536
AE104551	TGTAACACGACGGCCAGTCGGCACTTGACAAATCTGCTTC	1416	CGGAAACAGCTATGACCGCACTTCTGAGCAACCTG	1537
AE104552	TGTAACACGACGGCCAGTCGGCACTTGACAAATCTGCTTC	1417	CGGAAACAGCTATGACCGCACTTCTGAGCAACCTG	1538
AE104553	TGTAACACGACGGCCAGTCGGCACTTGACAAATCTGCTTC	1418	CGGAAACAGCTATGACCGCACTTCTGAGCAACCTG	1539
AE104554	TGTAACACGACGGCCAGTCGGCACTTGACAAATCTGCTTC	1419	CGGAAACAGCTATGACCGCACTTCTGAGCAACCTG	1540
AE104555	TGTAACACGACGGCCAGTCGGCACTTGACAAATCTGCTTC	1420	CGGAAACAGCTATGACCGCACTTCTGAGCAACCTG	1541
AE104556	TGTAACACGACGGCCAGTCGGCACTTGACAAATCTGCTTC	1421	CGGAAACAGCTATGACCGCACTTCTGAGCAACCTG	1542
AE104557	TGTAACACGACGGCCAGTCGGCACTTGACAAATCTGCTTC	1422	CGGAAACAGCTATGACCGCACTTCTGAGCAACCTG	1543
AE104558	TGTAACACGACGGCCAGTCGGCACTTGACAAATCTGCTTC	1423	CGGAAACAGCTATGACCGCACTTCTGAGCAACCTG	1544
AE104559	TGTAACACGACGGCCAGTCGGCACTTGACAAATCTGCTTC	1424	CGGAAACAGCTATGACCGCACTTCTGAGCAACCTG	1545

AE10782	TGTAAGACGACGCCAAGTCCTGACAGGCTCTGTCATC	1425	CAGGAACAGTATGACCAATTGAGGTCCACAA	1546
AE10783	TGTAAGACGCCAGTCCTGACAGGCTCTGTCATC	1426	CAGGAACAGTATGACCAATTGAGGTCCACAA	1547
AE10784	TGTAAGACGCCAGTCCTGACAGGCTCTGTCATC	1427	CAGGAACAGTATGACCAATTGAGGTCCACAA	1548
AE10785	TGTAAGACGCCAGTCCTGACAGGCTCTGTCATC	1428	CAGGAACAGTATGACCAATTGAGGTCCACAA	1549
AE10786	TGTAAGACGCCAGTCCTGACAGGCTCTGTCATC	1429	CAGGAACAGTATGACCAATTGAGGTCCACAA	1550
AE10981	TGTAAGACGCCAGTCCTGACAGGCTCTGTCATC	1430	CAGGAACAGTATGACCAATTGAGGTCCACAA	1551
AE10982	TGTAAGACGCCAGTCCTGACAGGCTCTGTCATC	1431	CAGGAACAGTATGACCAATTGAGGTCCACAA	1552
AE10983	TGTAAGACGCCAGTCCTGACAGGCTCTGTCATC	1432	CAGGAACAGTATGACCAATTGAGGTCCACAA	1553
AE10984	TGTAAGACGCCAGTCCTGACAGGCTCTGTCATC	1433	CAGGAACAGTATGACCAATTGAGGTCCACAA	1554
AE10985	TGTAAGACGCCAGTCCTGACAGGCTCTGTCATC	1434	CAGGAACAGTATGACCAATTGAGGTCCACAA	1555
AE10986	TGTAAGACGCCAGTCCTGACAGGCTCTGTCATC	1435	CAGGAACAGTATGACCAATTGAGGTCCACAA	1556
AE10987	TGTAAGACGCCAGTCCTGACAGGCTCTGTCATC	1436	CAGGAACAGTATGACCAATTGAGGTCCACAA	1557
AE10988	TGTAAGACGCCAGTCCTGACAGGCTCTGTCATC	1437	CAGGAACAGTATGACCAATTGAGGTCCACAA	1558
AE10989	TGTAAGACGCCAGTCCTGACAGGCTCTGTCATC	1438	CAGGAACAGTATGACCAATTGAGGTCCACAA	1559
AE11081	TGTAAGACGCCAGTCCTGACAGGCTCTGTCATC	1439	CAGGAACAGTATGACCAATTGAGGTCCACAA	1560
AE11080	TGTAAGACGCCAGTCCTGACAGGCTCTGTCATC	1440	CAGGAACAGTATGACCAATTGAGGTCCACAA	1561
AE110811	TGTAAGACGCCAGTCCTGACAGGCTCTGTCATC	1441	CAGGAACAGTATGACCAATTGAGGTCCACAA	1562
AE110812	TGTAAGACGCCAGTCCTGACAGGCTCTGTCATC	1442	CAGGAACAGTATGACCAATTGAGGTCCACAA	1563
AE11082	TGTAAGACGCCAGTCCTGACAGGCTCTGTCATC	1443	CAGGAACAGTATGACCAATTGAGGTCCACAA	1564
AE11083	TGTAAGACGCCAGTCCTGACAGGCTCTGTCATC	1444	CAGGAACAGTATGACCAATTGAGGTCCACAA	1565
AE11084	TGTAAGACGCCAGTCCTGACAGGCTCTGTCATC	1445	CAGGAACAGTATGACCAATTGAGGTCCACAA	1566
AE11085	TGTAAGACGCCAGTCCTGACAGGCTCTGTCATC	1446	CAGGAACAGTATGACCAATTGAGGTCCACAA	1567
AE11086	TGTAAGACGCCAGTCCTGACAGGCTCTGTCATC	1447	CAGGAACAGTATGACCAATTGAGGTCCACAA	1568
AE11087	TGTAAGACGCCAGTCCTGACAGGCTCTGTCATC	1448	CAGGAACAGTATGACCAATTGAGGTCCACAA	1569
AE11088	TGTAAGACGCCAGTCCTGACAGGCTCTGTCATC	1449	CAGGAACAGTATGACCAATTGAGGTCCACAA	1570
AE11089	TGTAAGACGCCAGTCCTGACAGGCTCTGTCATC	1450	CAGGAACAGTATGACCAATTGAGGTCCACAA	1571

Table XII  
Sample Description

Race	Cases			Controls			Total
	Angioedema	Angioedema-like	Total	Angioedema	Angioedema-like	Total	
Blacks	11	10	21	32	19	51	72
Caucasians	12	22	34	38	69	107	141
Other	0	1	1	0	1	1	2
Total	23	33	56	70	89	159	215

**Table XIII**  
**Candidate Angioedema Susceptibility Genes**

Chromosome	Gene	Gene ID
14	Bradykinin B2 Receptor	BDKRB2
19	Tissue Kallikrein	KLK1
X	Aminopeptidase P (Membrane Bound)	XPNPEP2

**Table XIV**  
**Association of SNPs of the present invention with Angioedema and/or Angioedema-like Events**

Gene ID	SNP ID	Sample or Subgroup	Scores Test	DF	Probability	Estimate Type	A,a <sup>1</sup>	Copies of Rare Allele (OR) <sup>2</sup>	OR	Upper 95% CL	OR
						Asymptotic	A,T	1	3.41	1.3238	8.7969
BDKRB2	AE104s9	Caucasians	7.01	2	0.0300	Exact					0.28
					0.0251	Exact					
KLK1	AE107s2	Blacks	7.50	2	0.0062	Asymptotic	C,T	1	5.64	1.4211	22.3807
					0.0062	Exact					0.09
XPNPEP2	AE100s4	Caucasians	13.44	2	0.0009	Exact	C,T	2	14.95	1.9838	+INF
		Angioedema-like	11.39	2	0.0022	Exact		2	10.82	1.3105	+INF
		Overall	10.72	2	0.0047	Asymptotic		2	11.11	1.2687	97.2709
											0.23

1 Most frequent (common) allele, least frequent (rare) allele.

2 The ratio of the odds of an adverse event (angioedema and/or Angioedema-like) in subjects carrying the specified number of copies of the rare allele, relative to controls matched for nationality, race, gender and starting dose, over the odds of such an adverse event for similarly matched subjects not carrying any copies of the rare allele.

3 Rare allele relative frequency.